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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/731,657
DATE: 11/29/2001
TIME: 15:35:50

Input Set : A:\09731657.raw.txt
Output Set: N:\CRF3\11292001\I731657.raw

ENTERED

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: OSTERHOFF, CAROLINE
6 IVELL, RICHARD
8 (ii) TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
10 (iii) NUMBER OF SEQUENCES: 11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
14 (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
15 (C) CITY: ARLINGTON
16 (D) STATE: VA
17 (E) COUNTRY: USA
18 (F) ZIP: 22201
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/731,657
C--> 28 (B) FILING DATE: 12-Mar-2001
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US/09/041,745
33 (B) FILING DATE:
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: SADOFF, B.J.
37 (B) REGISTRATION NUMBER: 36,663
38 (C) REFERENCE/DOCKET NUMBER: 35-125
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 703-816-4000
42 (B) TELEFAX: 703-816-4100
45 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 4665 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
53 (ii) MOLECULE TYPE: cdna
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..3114
59 (ix) FEATURE:
60 (A) NAME/KEY: 3'UTR
61 (B) LOCATION: 3115..4665
63 (ix) FEATURE:
64 (A) NAME/KEY: polyA-site

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65          (B) LOCATION: 4647..4652
66          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 AGC CAG CCC GAG GAC GCG AGC GGC AGG TGT GCA CAG AGG TTC TCC ACT      48
71 Ser Gln Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr
72 1          5          10          15
74 TTG TTT TCT GAA CTC GCG GTC AGG ATG GTT TTC TCT GTC AGG CAG TGT      96
75 Leu Phe Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys
76          20          25          30
78 GGC CAT GTT GGC AGA ACT GAA GAA GTT TTA CTG ACG TTC AAG ATA TTC      144
79 Gly His Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe
80          35          40          45
82 CTT GTC ATC ATT TGT CTT CAT GTC GTT CTG GTA ACA TCC CTG GAA GAA      192
83 Leu Val Ile Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu
84          50          55          60
86 GAT ACT GAT AAT TCC AGT TTG TCA CCA CCA CCT GCT AAA TTA TCT GTT      240
87 Asp Thr Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val
88 65          70          75          80
90 GTC AGT TTT GCC CCC TCC TCC AAT GAG GTT GAA ACA ACA AGC CTC AAT      288
91 Val Ser Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn
92          85          90          95
94 GAT GTT ACT TTA AGC TTA CTC CCT TCA AAC GAA ACA GAA AAA ACT AAA      336
95 Asp Val Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys
96          100          105          110
98 ATC ACT ATA GTA AAA ACC TTC AAT GCT TCA GGC GTC AAA CCC CAG AGA      384
99 Ile Thr Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg
100          115          120          125
102 AAT ATC TGC AAT TTG TCA TCT ATT TGC AAT GAC TCA GCA TTT TTT AGA      432
103 Asn Ile Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg
104          130          135          140
106 GGT GAG ATC ATG TTT CAA TAT GAT AAA GAA AGC ACT GTT CCC CAG AAT      480
107 Gly Glu Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn
108 145          150          155          160
110 CAA CAT ATA ACG AAT GGC ACC TTA ACT GGA GTC CTG TCT CTA AGT GAA      528
111 Gln His Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu
112          165          170          175
114 TTA AAA CGC TCA GAG CTC AAC AAA ACC CTG CAA ACC CTA AGT GAG ACT      576
115 Leu Lys Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr
116          180          185          190
118 TAC TTT ATA ATG TGT GCT ACA GCA GAG GCC CAA AGC ACA TTA AAT TGT      624
119 Tyr Phe Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys
120          195          200          205
122 ACA TTC ACA ATA AAA CTG AAT AAT ACA ATG AAT GCA TGT GCT GCA ATA      672
123 Thr Phe Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile
124          210          215          220
126 GCC GCT TTG GAA AGA GTA AAG ATT CGA CCA ATG GAA CAC TGC TGC TGT      720
127 Ala Ala Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys
128 225          230          235          240
130 TCT GTC AGG ATA CCC TGC CCT TCC TCC CCA GAA GAG TTG GGA AAG CTT      768
131 Ser Val Arg Ile Pro Cys Pro Ser Ser Pro Glu Glu Leu Gly Lys Leu

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132		245		250		255	
134	CAG TGT GAC CTG	CAG GAT CCC ATT GTC	TGT CTT GCT GAC	CAT CCA CGT		816	
135	Gln Cys Asp Leu	Gln Asp Pro Ile Val	Cys Leu Ala Asp	His Pro Arg			
136		260		265		270	
138	GGC CCA CCA TTT	TCT TCC AGC CAA	TCC ATC CCA GTG	GTG CCT CGG GCC		864	
139	Gly Pro Pro Phe	Ser Ser Ser Gln	Ser Ile Pro Val	Val Pro Arg Ala			
140		275		280		285	
142	ACT GTG CTT TCC	CAG GTC CCC AAA	GCT ACC TCT TTT	GCT GAG CCT CCA		912	
143	Thr Val Leu Ser	Gln Val Pro Lys	Ala Thr Ser Phe	Ala Glu Pro Pro			
144		290		295		300	
146	GAT TAT TCA CCT	GTG ACC CAC AAT	GTT CCC TCT CCA	ATA GGG GAG ATT		960	
147	Asp Tyr Ser Pro	Val Thr His Asn	Val Pro Ser Pro	Ile Gly Glu Ile			
148	305		310		315	320	
150	CAA CCC CTT TCA	CCC CAG CCT TCA	GCT CCC ATA GCT	TCC AGC CCT GCC		1008	
151	Gln Pro Leu Ser	Pro Gln Pro Ser	Ala Pro Ile Ala	Ser Ser Pro Ala			
152		325		330		335	
154	ATT GAC ATG CCC	CCA CAG TCT GAA	ACG ATC TCT TCC	CCT ATG CCC CAA		1056	
155	Ile Asp Met Pro	Pro Gln Ser Glu	Thr Ile Ser Ser	Pro Met Pro Gln			
156		340		345		350	
158	ACC CAT GTC TCC	GGC ACC CCA CCT	CCT GTG AAA GCC	TCA TTT TCC TCT		1104	
159	Thr His Val Ser	Gly Thr Pro Pro	Pro Val Lys Ala	Ser Phe Ser Ser			
160		355		360		365	
162	CCC ACC GTG TCT	GCC CCT GCG AAT	GTC AAC ACT ACC	AGC GCA CCT CCT		1152	
163	Pro Thr Val Ser	Ala Pro Ala Asn	Val Asn Thr Thr	Ser Ala Pro Pro			
164		370		375		380	
166	GTC CAG ACA GAC	ATC GTC AAC ACC	AGC AGT ATT TCT	GAT CTT GAG AAC		1200	
167	Val Gln Thr Asp	Ile Val Asn Thr	Ser Ser Ile Ser	Asp Leu Glu Asn			
168	385		390		395	400	
170	CAA GTG TTG CAG	ATG GAG AAG GCT	CTG TCC TTG GGC	AGC CTG GAG CCT		1248	
171	Gln Val Leu Gln	Met Glu Lys Ala	Leu Ser Leu Gly	Ser Leu Glu Pro			
172		405		410		415	
174	AAC CTC GCA GGA	GAA ATG ATC AAC	CAA GTC AGC AGA	CTC CTT CAT TCC		1296	
175	Asn Leu Ala Gly	Glu Met Ile Asn	Gln Val Ser Arg	Leu Leu His Ser			
176		420		425		430	
178	CCG CCT GAC ATG	CTG GCC CCT CTG	GCT CAA AGA TTG	CTG AAA GTA GTG		1344	
179	Pro Pro Asp Met	Leu Ala Pro Leu	Ala Gln Arg Leu	Leu Lys Val Val			
180		435		440		445	
182	GAT GAC ATT GGC	CTA CAG CTG AAC	TTT TCA AAC ACG	ACT ATA AGT CTA		1392	
183	Asp Asp Ile Gly	Leu Gln Leu Asn	Phe Ser Asn Thr	Thr Ile Ser Leu			
184		450		455		460	
186	ACC TCC CCT TCT	TTG GCT CTG GCT	GTG ATC AGA GTG	AAT GCC AGT AGT		1440	
187	Thr Ser Pro Ser	Leu Ala Leu Ala	Val Ile Arg Val	Asn Ala Ser Ser			
188	465		470		475	480	
190	TTC AAC ACA ACT	ACC TTT GTG GCC	CAA GAC CCT GCA	AAT CTT CAG GTT		1488	
191	Phe Asn Thr Thr	Thr Phe Val Ala	Gln Asp Pro Ala	Asn Leu Gln Val			
192		485		490		495	
194	TCT CTG GAA ACC	CAA GCT CCT GAG	AAC AGT ATT GGC	ACA ATT ACT CTT		1536	
195	Ser Leu Glu Thr	Gln Ala Pro Glu	Asn Ser Ile Gly	Thr Ile Thr Leu			
196		500		505		510	

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198	CCT TCA TCG CTG ATG AAT AAT TTA CCA GCT CAT GAC ATG GAG CTA GCT	1584
199	Pro Ser Ser Leu Met Asn Asn Leu Pro Ala His Asp Met Glu Leu Ala	
200	515 520 525	
202	TCC AGG GTT CAG TTC AAT TTT TTT GAA ACA CCT GCT TTG TTT CAG GAT	1632
203	Ser Arg Val Gln Phe Asn Phe Phe Glu Thr Pro Ala Leu Phe Gln Asp	
204	530 535 540	
206	CCT TCC CTG GAG AAC CTC TCT CTG ATC AGC TAC GTC ATA TCA TCG AGT	1680
207	Pro Ser Leu Glu Asn Leu Ser Leu Ile Ser Tyr Val Ile Ser Ser Ser	
208	545 550 555 560	
210	GTT GCA AAC CTG ACC GTC AGG AAC TTG ACA AGA AAC GTG ACA GTC ACA	1728
211	Val Ala Asn Leu Thr Val Arg Asn Leu Thr Arg Asn Val Thr Val Thr	
212	565 570 575	
214	TTA AAG CAC ATC AAC CCG AGC CAG GAT GAG TTA ACA GTG AGA TGT GTA	1776
215	Leu Lys His Ile Asn Pro Ser Gln Asp Glu Leu Thr Val Arg Cys Val	
216	580 585 590	
218	TTT TGG GAC TTG GGC AGA AAT GGT GGC AGA GGA GGC TGG TCA GAC AAT	1824
219	Phe Trp Asp Leu Gly Arg Asn Gly Gly Arg Gly Gly Trp Ser Asp Asn	
220	595 600 605	
222	GGC TGC TCT GTC AAA GAC AGG AGA TTG AAT GAA ACC ATC TGT ACC TGT	1872
223	Gly Cys Ser Val Lys Asp Arg Arg Leu Asn Glu Thr Ile Cys Thr Cys	
224	610 615 620	
226	AGC CAT CTA ACA AGC TTC GGC GTT CTG CTG GAC CTA TCT AGG ACA TCT	1920
227	Ser His Leu Thr Ser Phe Gly Val Leu Leu Asp Leu Ser Arg Thr Ser	
228	625 630 635 640	
230	GTG CTG CCT GCT CAA ATG ATG GCT CTG ACG TTC ATT ACA TAT ATT GGT	1968
231	Val Leu Pro Ala Gln Met Met Ala Leu Thr Phe Ile Thr Tyr Ile Gly	
232	645 650 655	
234	TGT GGG CTT TCA TCA ATT TTT CTG TCA GTG ACT CTT GTA ACC TAC ATA	2016
235	Cys Gly Leu Ser Ser Ile Phe Leu Ser Val Thr Leu Val Thr Tyr Ile	
236	660 665 670	
238	GCT TTT GAA AAG ATC CGG AGG GAT TAC CCT TCC AAA ATC CTC ATC CAG	2064
239	Ala Phe Glu Lys Ile Arg Arg Asp Tyr Pro Ser Lys Ile Leu Ile Gln	
240	675 680 685	
242	CTG TGT GCT GCT CTG CTT CTG CTG AAC CTG GTC TTC CTC CTG GAC TCG	2112
243	Leu Cys Ala Ala Leu Leu Leu Leu Asn Leu Val Phe Leu Leu Asp Ser	
244	690 695 700	
246	TGG ATT GCT CTG TAT AAG ATG CAA GGC CTC TGC ATC TCA GTG GCT GTA	2160
247	Trp Ile Ala Leu Tyr Lys Met Gln Gly Leu Cys Ile Ser Val Ala Val	
248	705 710 715 720	
250	TTT CTT CAT TAT TTT CTC TTG GTC TCA TTC ACA TGG ATG GGC CTA GAA	2208
251	Phe Leu His Tyr Phe Leu Leu Val Ser Phe Thr Trp Met Gly Leu Glu	
252	725 730 735	
254	GCA TTC CAT ATG TAC CTG GCC CTT GTC AAA GTA TTT AAT ACT TAC ATC	2256
255	Ala Phe His Met Tyr Leu Ala Leu Val Lys Val Phe Asn Thr Tyr Ile	
256	740 745 750	
258	CGA AAA TAC ATC CTT AAA TTC TGC ATT GTC GGT TGG GGG GTA CCA GCT	2304
259	Arg Lys Tyr Ile Leu Lys Phe Cys Ile Val Gly Trp Gly Val Pro Ala	
260	755 760 765	
262	GTG GTT GTG ACC ATC ATC CTG ACT ATA TCC CCA GAT AAC TAT GGG CTT	2352

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263	Val	Val	Val	Thr	Ile	Ile	Leu	Thr	Ile	Ser	Pro	Asp	Asn	Tyr	Gly	Leu	
264		770					775					780					
266	GGA	TCC	TAT	GGG	AAA	TTC	CCC	AAT	GGT	TCA	CCG	GAT	GAC	TTC	TGC	TGG	2400
267	Gly	Ser	Tyr	Gly	Lys	Phe	Pro	Asn	Gly	Ser	Pro	Asp	Asp	Phe	Cys	Trp	
268	785					790					795					800	
270	ATC	AAC	AAC	AAT	GCA	GTA	TTC	TAC	ATT	ACG	GTG	GTG	GGA	TAT	TTC	TGT	2448
271	Ile	Asn	Asn	Asn	Ala	Val	Phe	Tyr	Ile	Thr	Val	Val	Gly	Tyr	Phe	Cys	
272					805					810						815	
274	GTG	ATA	TTT	TTG	CTG	AAC	GTC	AGC	ATG	TTC	ATT	GTG	GTC	CTG	GTT	CAG	2496
275	Val	Ile	Phe	Leu	Leu	Asn	Val	Ser	Met	Phe	Ile	Val	Val	Leu	Val	Gln	
276				820					825					830			
278	CTC	TGT	CGA	ATT	AAA	AAG	AAG	AAG	CAA	CTG	GGA	GCC	CAG	CGA	AAA	ACC	2544
279	Leu	Cys	Arg	Ile	Lys	Lys	Lys	Lys	Gln	Leu	Gly	Ala	Gln	Arg	Lys	Thr	
280			835						840					845			
282	AGT	ATT	CAA	GAC	CTC	AGG	AGT	ATC	GCT	GGC	CTT	ACA	TTT	TTA	CTG	GGA	2592
283	Ser	Ile	Gln	Asp	Leu	Arg	Ser	Ile	Ala	Gly	Leu	Thr	Phe	Leu	Leu	Gly	
284		850				855						860					
286	ATA	ACT	TGG	GGC	TTT	GCC	TTC	TTT	GCC	TGG	GGA	CCA	GTT	AAC	GTG	ACC	2640
287	Ile	Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Val	Asn	Val	Thr	
288	865				870					875						880	
290	TTC	ATG	TAT	CTG	TTT	GCC	ATC	TTT	AAT	ACC	TTA	CAA	GGA	TTT	TTC	ATA	2688
291	Phe	Met	Tyr	Leu	Phe	Ala	Ile	Phe	Asn	Thr	Leu	Gln	Gly	Phe	Phe	Ile	
292				885						890						895	
294	TTC	ATC	TTT	TAC	TGT	GTG	GCC	AAA	GAA	AAT	GTC	AGG	AAG	CAA	TGG	AGG	2736
295	Phe	Ile	Phe	Tyr	Cys	Val	Ala	Lys	Glu	Asn	Val	Arg	Lys	Gln	Trp	Arg	
296				900					905					910			
298	CGG	TAT	CTT	TGT	TGT	GGA	AAG	TTA	CGG	CTG	GCT	GAA	AAT	TCT	GAC	TGG	2784
299	Arg	Tyr	Leu	Cys	Cys	Gly	Lys	Leu	Arg	Leu	Ala	Glu	Asn	Ser	Asp	Trp	
300			915					920						925			
302	AGT	AAA	ACT	GCT	ACT	AAT	GGT	TTA	AAG	AAG	CAG	ACT	GTA	AAC	CAA	GGA	2832
303	Ser	Lys	Thr	Ala	Thr	Asn	Gly	Leu	Lys	Lys	Gln	Thr	Val	Asn	Gln	Gly	
304		930				935					940						
306	GTG	TCC	AGC	TCT	TCA	AAT	TCC	TTA	CAG	TCA	AGC	AGT	AAC	TCC	ACT	AAC	2880
307	Val	Ser	Ser	Ser	Ser	Asn	Ser	Leu	Gln	Ser	Ser	Ser	Asn	Ser	Thr	Asn	
308	945				950					955						960	
310	TCC	ACC	ACA	CTG	CTA	GTG	AAT	AAT	GAT	TGC	TCA	GTA	CAC	GCA	AGC	GGG	2928
311	Ser	Thr	Thr	Leu	Leu	Val	Asn	Asn	Asp	Cys	Ser	Val	His	Ala	Ser	Gly	
312				965						970						975	
314	AAT	GGA	AAT	GCT	TCT	ACA	GAG	AGG	AAT	GGG	GTC	TCT	TTT	AGT	GTT	CAG	2976
315	Asn	Gly	Asn	Ala	Ser	Thr	Glu	Arg	Asn	Gly	Val	Ser	Phe	Ser	Val	Gln	
316				980					985					990			
318	AAT	GGA	GAT	GTG	TGC	CTT	CAC	GAT	TTC	ACT	GGA	AAA	CAG	CAC	ATG	TTT	3024
319	Asn	Gly	Asp	Val	Cys	Leu	His	Asp	Phe	Thr	Gly	Lys	Gln	His	Met	Phe	
320			995					1000						1005			
322	AAC	GAG	AAG	GAA	GAT	TCC	TGC	AAT	GGG	AAA	GGC	CGT	ATG	GCT	CTC	AGA	3072
323	Asn	Glu	Lys	Glu	Asp	Ser	Cys	Asn	Gly	Lys	Gly	Arg	Met	Ala	Leu	Arg	
324		1010				1015					1020						
326	AGG	ACT	TCA	AAG	CGG	GGA	AGC	TTA	CAC	TTT	ATT	GAG	CAA	ATG			3114
327	Arg	Thr	Ser	Lys	Arg	Gly	Ser	Leu	His	Phe	Ile	Glu	Gln	Met			

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11